

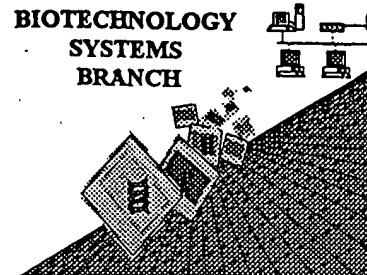
M. Garcia

RAW SEQUENCE LISTING **ERROR REPORT**

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MAY 30 2000

TECH CENTER 1600/2900



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

09/253,153

Art Unit / Team No. :

1627

Date Processed by STIC:

5/15/2000

#6

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

1627

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/253,153

DATE: 05/15/2000
TIME: 12:31:02

Does Not Comply
Corrected Diskette Needed

Input Set : A:\Schwabal.app
Output Set: N:\CRF3\05152000\I253153.raw

3 <110> APPLICANT: Schwabacher, Alan W.
5 <120> TITLE OF INVENTION: One-Dimensional Compound Arrays and a Method for
6 Assaying Them
8 <130> FILE REFERENCE: Schwabacher-One-Dimensional Arrays
10 <140> CURRENT APPLICATION NUMBER: 09/253,153
11 <141> CURRENT FILING DATE: 1999-02-19
13 <150> PRIOR APPLICATION NUMBER: 60/075,629
14 <151> PRIOR FILING DATE: 1998-02-21
16 <160> NUMBER OF SEQ ID NOS: 3
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 7
22 <212> TYPE: PRT
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Description of Artificial Sequence: Sequence of
27 amino acids synthesized on string
29 <400> SEQUENCE: 1
30 His Pro Gln Phe Ala Ala Ala
31 1 5
34 <210> SEQ ID NO: 2
35 <211> LENGTH: 8
36 <212> TYPE: PRT
37 <213> ORGANISM: Artificial Sequence
39 <220> FEATURE:
40 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
41 synthesized on string
43 <400> SEQUENCE: 2
W--> 44 Xaa Xaa Pro Gln Phe Ala Ala Ala
45 1 5
48 <210> SEQ ID NO: 3
49 <211> LENGTH: 8
50 <212> TYPE: PRT
51 <213> ORGANISM: Artificial Sequence
53 <220> FEATURE:
54 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
55 synthesized on string
57 <400> SEQUENCE: 3
W--> 58 Xaa His Pro Gln Phe Ala Ala Ala
59 1 5

See item 10 on Ena Summary Sheet

See 10

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/253,153

DATE: 05/15/2000

TIME: 12:31:03

Input Set : A:\Schwabal.app

Output Set: N:\CRF3\05152000\I253153.raw

L:44 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:44 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:44 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:58 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:58 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:58 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/253,153

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) **(2) INFORMATION FOR SEQ ID NO:X:**
 (i) **SEQUENCE CHARACTERISTICS:**(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) **SEQUENCE DESCRIPTION:SEQ ID NO:X:**
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) **<210> sequence id number**
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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